structure databases, homology modeling, molecular modeling, de novo protein folding, computational protein structure prediction, *ab initio* methods and combinations thereof.

43. (New) The method of claim 42, wherein the experimental methods include x-ray crystallography and NMR spectroscopy.

44. (New) The method of claim 23, wherein the step of generating 3-D protein structural variant models from the sequences is performed by a combination of homology modeling and *ab initio* methods.

45. (New) The method of claim 23, wherein the database further comprises 3-D molecular structural data of structural variant models.

46. (New) The method of claim 41, wherein the step of generating 3-D protein structural variant models from the sequences is performed by a method selected from the group consisting of experimental methods, searching protein structure databases, homology modeling, molecular modeling, de novo protein folding, computational protein structure prediction, *ab initio* methods and combinations thereof.

B1 cont

47. (New) The method of claim 46, wherein the experimental methods include x-ray crystallography and NMR spectroscopy.

48. (New) The method of claim 41, wherein the step of generating 3-D protein structural variant models from the sequences is performed by a combination of homology modeling and *ab initio* methods.

49. (New) The method of claim 41, wherein the database further comprises 3-D molecular structural data of structural variant models.

Please replace claim 23 with amended claim 23 as follows:

---

23. (Amended) A computer-based method for predicting clinical responses in patients based on genetic polymorphisms, comprising:

B2

obtaining one or more amino acid sequences for a target protein that is the product of a gene exhibiting genetic polymorphisms;

generating 3-D protein structural variant models from the sequences;